

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGGTGTGA	60
ATTGTATAGC AATATTTTGG AGATTACAGA GTTTAGTAA TTACCAATTAA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTAAATGT GAATTGACCA TTATCCTTTA	240
AAAGCTTCA AAANAAANAA TTATTGAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAN AACTGAAGGG CANAAAGAAT TAATTTTAC TTCAATGAAAC NCACCCANAT	360
TTACAATGGC TTAATGCAAN GGAAAAGCA GTGGAAGTAGC GGAAGTANTC AAGGTCTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTITTAAGG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTCTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAAATC ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAAG GGGACAAAGG CTAATCCAA	240
AAACATCAAAG AAAGGAAGGT GGCCTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGAGGAC AGTGGAGGAA CAACTGACCA TGTCAGGAGG CTCCTGTGTG	360
CTGGCTCTG GTCTTCAGCC CCCAGCTCTG GAAGGCCACC CTCTGCTGAT CCTGGTGGC	420
CCACACTCCT TGAACACACCA TCCCCAGGTT ATATTCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCCTG CTCCCTGAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCC AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACCTCTAT GGNCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs



PCT

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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :  C07K 14/00, A61K 39/00		A2	(11) International Publication Number: WO 98/37093  (43) International Publication Date: 27 August 1998 (27.08.98)									
<p>(21) International Application Number: PCT/US98/03492</p> <p>(22) International Filing Date: 25 February 1998 (25.02.98)</p> <p>(30) Priority Data:</p> <table> <tr> <td>08/806,099</td> <td>25 February 1997 (25.02.97)</td> <td>US</td> </tr> <tr> <td>08/904,804</td> <td>1 August 1997 (01.08.97)</td> <td>US</td> </tr> <tr> <td>09/020,956</td> <td>9 February 1998 (09.02.98)</td> <td>US</td> </tr> </table> <p>(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).</p> <p>(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).</p> <p>(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).</p>		08/806,099	25 February 1997 (25.02.97)	US	08/904,804	1 August 1997 (01.08.97)	US	09/020,956	9 February 1998 (09.02.98)	US	<p>(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i></p>	
08/806,099	25 February 1997 (25.02.97)	US										
08/904,804	1 August 1997 (01.08.97)	US										
09/020,956	9 February 1998 (09.02.98)	US										
<p>(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE</p> <p>(57) Abstract</p> <p>Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.</p>												

ACCCAAAAAT	CCAATGCTGA	ATATTTGGCT	TCATTATTCC	CANATTCTTT	GATTGTCAA	60
GGATTTAATG	TTGCTCAGC	TTGGGCACCT	CAGTTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
TTTATATAT	CGAGCAACAA	TATTCAGCG	CGACAAACAGG	TTATTGAACT	TGCCGCCAG	180
TTNAATTCA	TTCCCATGTA	CTTGGGATCC	TTATCATCAG	CCAGAGAGAT	TGAAAATTAA	240
CCCCTACNAC	TCTTTACTCT	CTGGANAGGG	CCAGTGGTGG	TAGCTATAAG	CTTGGCCACA	300
TTTTTTTTTC	CTTTATTCC	TTGTCAGA				328

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAAACT	TCTCCCTCAT	TCCAAGAGTT	180
TCTAATATT	GCATGAACCT	GCTGATAANC	CATGTTAANA	AACAATATC	TCTCTNACCT	240
TCTCATCGGT						250

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAAC	TCATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTG	ATTGTCAAAG	60
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TTTATATATG	CAGCAACAA	ATTCAAGCGC	GACAACAGGT	TATTGAACCTT	GCCCCGCAGT	180
TGAATTTCAT	TCCCATTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTAC	240
CCCTACGACT	CTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTCC	TTTATTCC	TGTCAGAGAT	CCGATTTCATC	CATATGCTAN	AAACCAACAG	360
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ACTTGCTCT	CCCTAATATA	CCTC				444

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120

CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AACCGAGGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAAC <del>C</del> AGGT	TTCCAACCA	GGTGGAAATC	TCCTATACTT	360
GGTGCC						366

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCAANGAGGG	AGGGCCGGGC	CAGGAGAAC	TCCGCTTGT	60
CAAGACAGGG	GCCTAAGGG	GGTCTCCACA	CTGCTNNTAA	GGGCTNTTNC	ATTTTTTAT	120
TAATAAAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTTCCC	TTNGGCTGGA	AAATTTAAA	180
ATCAAAAATT	TCTCTNAAGTT	NTCAAGCTAT	CATAATAC	NTATCCTGAA	AAAGCAACAT	240
AATTCTTCCT	TCCCTCCTTT					260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG	GTAAGTTTAN	AAATGTTATA	ATTTCAAGAA	NAGGAACGCA	TATAATTGTA	60
TCTTGCTAT	AATTTTCTAT	TTTAATAAGG	AAATAGCAA	TTGGGGTGGG	GGGAATGTAG	120
GGCATTCTAC	AGTTTGAGCA	AAATGCAATT	AAATGTGGAA	GGACAGCACT	GAAAAATT	180
ATGAATAATC	TGTATGATTA	TATGCTCTA	GAGTAGATT	ATAATTAGCC	ACTTACCTA	240
ATATCCCTCA	TGCTTGAAA	GT				262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG	TGCATTACCG	GAANTGGATC	AANGACACCA	TCGTGGCCAA	CCCCCTGAGCA	60
CCCTATCAA	CTCCCTTTTG	TAGTAAACTT	GGAACCTTGG	AAATGACCA	GCCAAGACTC	120
AGGCCTCCCC	AGTTCTACTG	ACCTTTGTCC	TTANGTNTNA	NGTCCAGGGT	TGCTAGGAAA	180
ANAAATCAGC	AGACACAGGT	GTAAA				205

## (2) INFORMATION FOR SEQ ID NO:219:

Hit [ENTER] to continue ...:

'!NA\_SEQUENCE 1.0

ID AA447322 standard; RNA; EST; 618 BP.

XX

AC AA447322;

XX

SV AA447322;1

XX

DT 07-APR-1998 (Rel. 55, Created).

DT 07-APR-1998 (Rel. 55, Last updated, Version 1)

XX

DE SA.C08R PN001-Normal Human Prostate Homo sapiens cDNA clone SA.C08

DE 5'.

XX

KW EST.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;

OC Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-618

RX MEDLINE; 98126432.

RA Nelson P.S., Ng W.-L., Schummer M., True L.D., Liu A.L., Bumgarner R..

RA Ferguson C., Dimak A., Hood L.;

RT "An expressed-sequence-tag database of the human prostate: sequence analysis of 1168 cDNA clones";

RL Genomics 47(1):12-25(1998).

XX

CC Contact: Nelson PS

CC Department of Molecular Biotechnology

CC University of Washington

CC Box 357730, HSB K360, 1705 NE Pacific, Seattle, WA 98195, USA

CC Tel: 206 685 7336

CC Fax: 206 685 7301

CC Email: psnels@u.washington.edu

CC Seq primer: M13 Reverse.

XX

FH Key Location/Qualifiers

FH

FT source 1. .618

FT /db\_xref="taxon:9606"

FT /db\_xref="ESTLIB:876"

FT /note="Organ: prostate; Vector: pSport1; Site\_1: Not1;

FT Site\_2: Sal1; PolyA+ RNA was isolated from the prostate of

FT a healthy 25 year old male organ donor. 1st strand cDNA

FT was primed with oligo(dT)Not1. Double-stranded cDNA was

FT ligated to Sal1 adapters and directionally cloned into

FT pSport1 (Life Technologies). Average insert size is 1.1kb."

FT /sex="male"

FT /organism="Homo sapiens"

FT /clone="SA.C08"

FT /clone\_lib="PN001-Normal Human Prostate"

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SQ Sequence 618 BP; 165 A; 141 C; 118 G; 192 T; 2 other;

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101 ACTTTCTAAA TTATTGAATT TCCATCATGC ATTCATCCAA AATTAAGGCA  
151 GACTGTTGG ATTCTTCCAG TGGCCAGATG AGCTAAATTA AATCACAAAA  
201 GCAGATGCTT TTGTATGATC TCCAAATTGC CAACTTTAAG GAAATATTCT  
251 CTTGAAATTG TCTTTAAAGA TCTTTGCAG CTTTGAGAT ACCCAGACTG  
301 AGCTGGAACG GGAATTGTC TTCTTATTGA CTCTACTTCT TTAAAAGCGG  
351 CTGCCCATTA CATTCCCTAG CTGTCCTTGC AGTTAGGTGT ACATGTGACT  
401 GAGTGTGGC CAGTGAGATG AAGTCTCCTC AAAGGAAGGC AGCATGTGTC  
451 CTTTTCATC CCNGCATCTT GCTGCTGGGA TTGTGGATAT AACAGGAGCC  
501 CTGGCAGCTG TCTCCAGAGG ATCAAAGCCA CACCCAAAGA GTAAGGCAGA  
551 TTAGAGACCA GANAGACCTT GACTACTTCC CTACTTCCAC TGCTTTTCC  
601 TGCATTAAGC CATGTAAA

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XP 211400

IDS

Hit [ENTER] to continue ...:

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XX  
SV AA447322;1  
XX  
DT 07-APR-1998 (Rel. 55, Created).  
DT 07-APR-1998 (Rel. 55, Last updated, Version 1)  
XX  
DE SA.C08R PN001-Normal Human Prostate Homo sapiens cDNA clone SA.C08  
DE 5'.  
XX  
KW EST.  
XX  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;  
OC Primates; Catarrhini; Hominidae; Homo.  
XX  
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RP 1-618  
RX MEDLINE; 98126432.  
RA Nelson P.S., Ng W.-L., Schummer M., True L.D., Liu A.L., Bumgarner R.,  
RA Ferguson C., Dimak A., Hood L.;  
RT "An expressed-sequence-tag database of the human prostate: sequence  
analysis of 1168 cDNA clones";  
RL Genomics 47(1):12-25(1998).  
XX  
CC Contact: Nelson PS  
CC Department of Molecular Biotechnology  
CC University of Washington  
CC Box 357730, HSB K360, 1705 NE Pacific, Seattle, WA 98195, USA  
CC Tel: 206 685 7336  
CC Fax: 206 685 7301  
CC Email: psnels@u.washington.edu  
CC Seq primer: M13 Reverse.  
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FH Key Location/Qualifiers  
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FT source 1. .618  
FT /db\_xref="taxon:9606"  
FT /db\_xref="ESTLIB:876"  
FT /note="Organ: prostate; Vector: pSport1; Site\_1: Not1;  
FT Site\_2: Sal1; PolyA+ RNA was isolated from the prostate of  
FT a healthy 25 year old male organ donor. 1st strand cDNA  
FT was primed with oligo(dT)Not1. Double-stranded cDNA was  
FT ligated to Sal1 adapters and directionally cloned into  
FT pSport1 (Life Technologies). Average insert size is 1.1kb."  
FT /sex="male"  
FT /organism="Homo sapiens"  
FT /clone="SA.C08"  
FT /clone\_lib="PN001-Normal Human Prostate"  
XX  
SQ Sequence 618 BP; 165 A; 141 C; 118 G; 192 T; 2 other;

Aa447322 Length: 618 November 9, 1999 11:49 Type: N Check: 7801 ..

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1 CGACCCACGC GTCCGCCACG CGTCCGGCTT AATTCAGAG ATTCTTTCCA  
51 TATGTTACTA AAAATGTTT TGTTCAGCCT AACATACTGA GTTTTTTTA  
101 ACTTTCTAAA TTATTGAATT TCCATCATGC ATTCACTCAA AATTAAGGCA  
151 GACTGTTGG ATTCTTCCAG TGGCCAGATG AGCTAAATTA AATCACAAAA  
201 GCAGATGCTT TTGTATGATC TCCAAATTGC CAACTTTAAG GAAATATTCT  
251 CTTGAAATTG TCTTTAAAGA TCTTTGCAG CTTTGCAGAT ACCCAGACTG  
301 AGCTGGAACG GGAATTGTC TTCCTATTGA CTCTACTTCT TTAAAAGCGG  
351 CTGCCATTAA CATTCTCAG CTGTCCTTGC AGTTAGGTGT ACATGTGACT  
401 GAGTGTTGGC CAGTGAGATG AAGTCTCCTC AAAGGAAGGC AGCATGTGTC  
451 CTTTTTCATC CCNGCATCTT GCTGCTGGGA TTGTGGATAT AACAGGAGCC  
501 CTGGCAGCTG TCTCCAGAGG ATCAAAGCCA CACCCAAAGA GTAAGGCAGA  
551 TTAGAGACCA GANAGACCTT GACTACTTCC CTACTTCCAC TGCTTTTCC  
601 TGCATTAAGC CATGTAAA

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